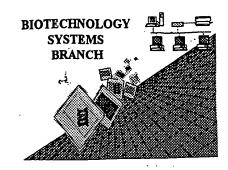# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/830,400_

Source: _PCT/09_

Date Processed by STIC: _8/30/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/830,400

DATE: 08/30/2001
TIME: 10:04:17

Input Set : A:\Es.txt
Output Set: N:\CRF3\08302001\I830400.raw

Does Not Comply
Corrected Diskette Needed

pp 1-3

```
 4 <110> APPLICANT: Nadler, Lee M.
 5        Hahn, William C.
 6        Schultz, Joachim L.
 7        Vonderheide, Robert H.
10 <120> TITLE OF INVENTION: CANCER IMMUNOTHERAPY AND DIAGNOSIS USING
11        UNIVERSAL TUMOR ASSOCIATED ANTIGENS, SUCH AS THE TELOMERASE
12        CATALYTIC SUBUNIT (hTERT), AND METHODS FOR IDENTIFYING
13        UNIVERSAL TUMOR ASSOCIATED ANTIGENS
16 <130> FILE REFERENCE: 50059/007002
18 <140> CURRENT APPLICATION NUMBER: US 09/830,400
19 <141> CURRENT FILING DATE: 2001-04-25
21 <150> PRIOR APPLICATION NUMBER: PCT/US99/25438
22 <151> PRIOR FILING DATE: 1999-10-29
24 <150> PRIOR APPLICATION NUMBER: US 60/106,106
25 <151> PRIOR FILING DATE: 1998-10-29
27 <160> NUMBER OF SEQ ID NOS: 72
29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

ERRORED SEQUENCES

(global error)

insert a hard return after last amino acid

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      31 <210> SEQ ID NO: 1
      32 <211> LENGTH: 9
      33 <212> TYPE: PRT
      34 <213> ORGANISM: Homo sapiens
      36 <400> SEQUENCE: 1
E--> 37 Ile Leu Ala Lys Phe Leu His Trp Leu 1          5
      39 <210> SEQ ID NO: 2
      40 <211> LENGTH: 9
      41 <212> TYPE: PRT
      42 <213> ORGANISM: Homo sapiens
      44 <400> SEQUENCE: 2
E--> 45 Lys Leu Phe Gly Val Leu Arg Leu Lys 1          5
      47 <210> SEQ ID NO: 3
      48 <211> LENGTH: 9
      49 <212> TYPE: PRT
      50 <213> ORGANISM: Homo sapiens
      52 <400> SEQUENCE: 3
E--> 53 Glu Leu Leu Arg Ser Phe Phe Tyr Val 1          5
      55 <210> SEQ ID NO: 4
      56 <211> LENGTH: 9
      57 <212> TYPE: PRT
      58 <213> ORGANISM: Homo sapiens
      60 <400> SEQUENCE: 4
E--> 61 Arg Leu Val Asp Asp Phe Leu Leu Val 1          5
      63 <210> SEQ ID NO: 5
      64 <211> LENGTH: 9
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/830,400

DATE: 08/30/2001
TIME: 10:04:17

Input Set : A:\Es.txt
Output Set: N:\CRF3\08302001\I830400.raw

```
        65 <212> TYPE: PRT
        66 <213> ORGANISM: Homo sapiens
        68 <400> SEQUENCE: 5
E--> 69 Phe Leu Trp Gly Pro Arg Ala Leu Val 1                    5
        71 <210> SEQ ID NO: 6
        72 <211> LENGTH: 9
        73 <212> TYPE: PRT
        74 <213> ORGANISM: Homo sapiens
        76 <400> SEQUENCE: 6
E--> 77 His Phe Leu Leu Trp Lys Leu Ile Ala 1                    5
        79 <210> SEQ ID NO: 7
        80 <211> LENGTH: 9
        81 <212> TYPE: PRT
        82 <213> ORGANISM: Homo sapiens
        84 <400> SEQUENCE: 7
E--> 85 Ala His Thr Lys Asp Gly Phe Asn Phe 1                    5
        87 <210> SEQ ID NO: 8
        88 <211> LENGTH: 10
        89 <212> TYPE: PRT
        90 <213> ORGANISM: Homo sapiens
        92 <400> SEQUENCE: 8
E--> 93 Lys Leu Thr Arg His Arg Val Thr Tyr Val 1            5            10
        95 <210> SEQ ID NO: 9
        96 <211> LENGTH: 10
        97 <212> TYPE: PRT
        98 <213> ORGANISM: Homo sapiens
       100 <400> SEQUENCE: 9
E--> 101 Leu Leu Leu Asp Thr Arg Thr Leu Glu Val 1           5            10
       103 <210> SEQ ID NO: 10
       104 <211> LENGTH: 10
       105 <212> TYPE: PRT
       106 <213> ORGANISM: Homo sapiens
       108 <400> SEQUENCE: 10
E--> 109 Phe Leu His Trp Leu Met Ser Val Tyr Val 1           5            10
       111 <210> SEQ ID NO: 11
       112 <211> LENGTH: 10
       113 <212> TYPE: PRT
       114 <213> ORGANISM: Homo sapiens
       116 <400> SEQUENCE: 11
E--> 117 Phe Leu Leu Lys Leu Thr Arg His Arg Val 1           5            10
       119 <210> SEQ ID NO: 12
       120 <211> LENGTH: 10
       121 <212> TYPE: PRT
       122 <213> ORGANISM: Homo sapiens
       124 <400> SEQUENCE: 12
E--> 125 Trp Leu Met Ser Val Tyr Val Val Glu Leu 1           5            10
       127 <210> SEQ ID NO: 13
       128 <211> LENGTH: 10
       129 <212> TYPE: PRT
```

Input Set : **A:\Es.txt**
Output Set: **N:\CRF3\08302001\I830400.raw**

```
        130 <213> ORGANISM: Homo sapiens
        132 <400> SEQUENCE: 13
E--> 133 Gly Leu Phe Asp Val Phe Leu Arg Phe Met 1              5              10
        135 <210> SEQ ID NO: 14
        136 <211> LENGTH: 9
        137 <212> TYPE: PRT
        138 <213> ORGANISM: Homo sapiens
        140 <400> SEQUENCE: 14
E--> 141 Leu Leu Ala Arg Cys Ala Leu Phe Val 1                  5
        143 <210> SEQ ID NO: 15
        144 <211> LENGTH: 9
        145 <212> TYPE: PRT
        146 <213> ORGANISM: Homo sapiens
        148 <400> SEQUENCE: 15
E--> 149 Trp Leu Cys His Gln Ala Phe Leu Leu 1                  5
        151 <210> SEQ ID NO: 16
        152 <211> LENGTH: 10
        153 <212> TYPE: PRT
        154 <213> ORGANISM: Homo sapiens
        156 <400> SEQUENCE: 16
E--> 157 Val Glu Leu Leu Arg Ser Phe Phe Tyr Val 1             5              10
        159 <210> SEQ ID NO: 17
        160 <211> LENGTH: 9
        161 <212> TYPE: PRT
        162 <213> ORGANISM: Homo sapiens
        164 <400> SEQUENCE: 17
E--> 165 Phe Leu Trp Gly Pro Arg Ala Leu Val 1                  5
        167 <210> SEQ ID NO: 18
        168 <211> LENGTH: 9
        169 <212> TYPE: PRT
        170 <213> ORGANISM: Homo sapiens
        172 <400> SEQUENCE: 18
E--> 173 Leu Leu Phe Gly Tyr Pro Val Tyr Val 1                  5
        175 <210> SEQ ID NO: 19
        176 <211> LENGTH: 9
        177 <212> TYPE: PRT
        178 <213> ORGANISM: Homo sapiens
        180 <400> SEQUENCE: 19
E--> 181 Phe Leu Trp Gly Pro Arg Ala Leu Val 1                  5
        183 <210> SEQ ID NO: 20
        184 <211> LENGTH: 9
        185 <212> TYPE: PRT
        186 <213> ORGANISM: Homo sapiens
        188 <400> SEQUENCE: 20
E--> 189 Gly Ile Leu Gly Phe Val Phe Thr Leu 1                  5
```

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Input Set : **A:\Es.txt**
Output Set: **N:\CRF3\08302001\I830400.raw**

```
L:37 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:1
L:45 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:2
L:53 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:3
L:61 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:4
L:69 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:5
L:77 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:6
L:85 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:7
L:93 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:8
L:101 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:9
L:109 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:10
L:117 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:11
L:125 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:12
L:133 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:13
L:141 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:14
L:149 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:15
L:157 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:16
L:165 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:17
L:173 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:18
L:181 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:19
L:189 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:20
L:197 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:21
L:205 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:22
L:213 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:23
L:221 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:24
L:229 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:25
L:237 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:26
L:245 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:27
L:253 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:28
L:261 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:29
L:269 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:30
L:277 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:31
L:285 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:32
L:293 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:33
L:301 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:34
L:309 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:35
L:317 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:36
L:325 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:37
L:333 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:38
L:341 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:39
L:349 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:40
L:357 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:41
L:365 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:42
L:373 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:43
L:381 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:44
L:389 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:45
L:397 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:46
L:405 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:47
L:413 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:48
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Input Set : **A:\Es.txt**
Output Set: **N:\CRF3\08302001\I830400.raw**

L:421 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:49
L:429 M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:50